

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 09/602,800A
Source: IFW16
Date Processed by STIC: 12/28/2005

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 12/28/2005

PATENT APPLICATION: US/09/602,800A

TIME: 13:19:49

Input Set : A:\39766-0142 App09602800 saved Dec 21 2005.txt

Output Set: N:\CRF4\12282005\I602800A.raw

```

3 <110> APPLICANT: Sliwkowski, Mark X.
5 <120> TITLE OF INVENTION: TREATING PROSTATE CANCER WITH ANTI-ErbB2 ANTIBODIES
7 <130> FILE REFERENCE: 39766-0142D1
9 <140> CURRENT APPLICATION NUMBER: US 09/602,800A
10 <141> CURRENT FILING DATE: 2000-06-23
12 <150> PRIOR APPLICATION NUMBER: US 60/141,315
13 <151> PRIOR FILING DATE: 1999-06-25
15 <160> NUMBER OF SEQ ID NOS: 22
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 107
19 <212> TYPE: PRT
20 <213> ORGANISM: Mus musculus
22 <400> SEQUENCE: 1
23  Asp Thr Val Met Thr Gln Ser His Lys Ile Met Ser Thr Ser Val
24      1                      5                      10                      15
26  Gly Asp Arg Val Ser Ile Thr Cys Lys Ala Ser Gln Asp Val Ser
27                      20                      25                      30
29  Ile Gly Val Ala Trp Tyr Gln Gln Arg Pro Gly Gln Ser Pro Lys
30                      35                      40                      45
32  Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Asp
33                      50                      55                      60
35  Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile
36                      65                      70                      75
38  Ser Ser Val Gln Ala Glu Asp Leu Ala Val Tyr Tyr Cys Gln Gln
39                      80                      85                      90
41  Tyr Tyr Ile Tyr Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu
42                      95                      100                      105
44  Ile Lys
47 <210> SEQ ID NO: 2
48 <211> LENGTH: 119
49 <212> TYPE: PRT
50 <213> ORGANISM: Mus musculus
52 <400> SEQUENCE: 2
53  Glu Val Gln Leu Gln Gln Ser Gly Pro Glu Leu Val Lys Pro Gly
54      1                      5                      10                      15
56  Thr Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Phe Thr Phe Thr
57                      20                      25                      30
59  Asp Tyr Thr Met Asp Trp Val Lys Gln Ser His Gly Lys Ser Leu
60                      35                      40                      45
62  Glu Trp Ile Gly Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr
63                      50                      55                      60
65  Asn Gln Arg Phe Lys Gly Lys Ala Ser Leu Thr Val Asp Arg Ser
66                      65                      70                      75

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```

68 Ser Arg Ile Val Tyr Met Glu Leu Arg Ser Leu Thr Phe Glu Asp
69           80           85           90
71 Thr Ala Val Tyr Tyr Cys Ala Arg Asn Leu Gly Pro Ser Phe Tyr
72           95          100          105
74 Phe Asp Tyr Trp Gly Gln Gly Thr Thr Leu Thr Val Ser Ser
75          110          115
77 <210> SEQ ID NO: 3
78 <211> LENGTH: 107
79 <212> TYPE: PRT
80 <213> ORGANISM: Artificial Sequence
82 <220> FEATURE:
83 <223> OTHER INFORMATION: Consensus Amino Acid Sequence
85 <400> SEQUENCE: 3
86 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
87   1           5           10           15
89 Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asp Val Ser
90           20           25           30
92 Ile Gly Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
93           35           40           45
95 Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Thr Gly Val Pro Ser
96           50           55           60
98 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
99           65           70           75
101 Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
102           80           85           90
104 Tyr Tyr Ile Tyr Pro Tyr Thr Phe Gly Gln Gly Thr Lys Val Glu
105           95          100          105
107 Ile Lys
110 <210> SEQ ID NO: 4
111 <211> LENGTH: 119
112 <212> TYPE: PRT
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <223> OTHER INFORMATION: Consensus Amino Acid Sequence
118 <400> SEQUENCE: 4
119 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
120   1           5           10           15
122 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Thr
123           20           25           30
125 Asp Tyr Thr Met Asp Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
126           35           40           45
128 Glu Trp Val Ala Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr
129           50           55           60
131 Asn Gln Arg Phe Lys Gly Arg Phe Thr Leu Ser Val Asp Arg Ser
132           65           70           75
134 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
135           80           85           90
137 Thr Ala Val Tyr Tyr Cys Ala Arg Asn Leu Gly Pro Ser Phe Tyr
138           95          100          105

```

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```

140 Phe Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
141             110             115
143 <210> SEQ ID NO: 5
144 <211> LENGTH: 107
145 <212> TYPE: PRT
146 <213> ORGANISM: Homo sapiens
148 <400> SEQUENCE: 5
149 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val
150 1             5             10             15
152 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Ser Ile Ser
153             20             25             30
155 Asn Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys
156             35             40             45
158 Leu Leu Ile Tyr Ala Ala Ser Ser Leu Glu Ser Gly Val Pro Ser
159             50             55             60
161 Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile
162             65             70             75
164 Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln Gln
165             80             85             90
167 Tyr Asn Ser Leu Pro Trp Thr Phe Gly Gln Gly Thr Lys Val Glu
168             95             100            105
170 Ile Lys
173 <210> SEQ ID NO: 6
174 <211> LENGTH: 119
175 <212> TYPE: PRT
176 <213> ORGANISM: Homo sapiens
178 <400> SEQUENCE: 6
179 Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Gln Pro Gly
180 1             5             10             15
182 Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser
183             20             25             30
185 Ser Tyr Ala Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu
186             35             40             45
188 Glu Trp Val Ala Val Ile Ser Gly Asp Gly Gly Ser Thr Tyr Tyr
189             50             55             60
191 Ala Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser
192             65             70             75
194 Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Arg Ala Glu Asp
195             80             85             90
197 Thr Ala Val Tyr Tyr Cys Ala Arg Gly Arg Val Gly Tyr Ser Leu
198             95             100            105
200 Tyr Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser
201             110            115
203 <210> SEQ ID NO: 7
204 <211> LENGTH: 10
205 <212> TYPE: PRT
206 <213> ORGANISM: Mus musculus
208 <220> FEATURE:
209 <221> NAME/KEY: VARIANT

```

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Output Set: N:\CRF4\12282005\I602800A.raw

```

210 <222> LOCATION: 10
211 <223> OTHER INFORMATION: Xaa = D or S
213 <400> SEQUENCE: 7
W--> 214 Gly Phe Thr Phe Thr Asp Tyr Thr Met Xaa
215      1              5              10
217 <210> SEQ ID NO: 8
218 <211> LENGTH: 17
219 <212> TYPE: PRT
220 <213> ORGANISM: Mus musculus
222 <400> SEQUENCE: 8
223 Asp Val Asn Pro Asn Ser Gly Gly Ser Ile Tyr Asn Gln Arg Phe
224      1              5              10              15
226 Lys Gly
229 <210> SEQ ID NO: 9
230 <211> LENGTH: 10
231 <212> TYPE: PRT
232 <213> ORGANISM: Mus musculus
234 <400> SEQUENCE: 9
235 Asn Leu Gly Pro Ser Phe Tyr Phe Asp Tyr
236      1              5              10
238 <210> SEQ ID NO: 10
239 <211> LENGTH: 11
240 <212> TYPE: PRT
241 <213> ORGANISM: Mus musculus
243 <400> SEQUENCE: 10
244 Lys Ala Ser Gln Asp Val Ser Ile Gly Val Ala
245      1              5              10
247 <210> SEQ ID NO: 11
248 <211> LENGTH: 7
249 <212> TYPE: PRT
250 <213> ORGANISM: Mus musculus
252 <220> FEATURE:
253 <221> NAME/KEY: VARIANT
254 <222> LOCATION: 5
255 <223> OTHER INFORMATION: Xaa = R or L
257 <220> FEATURE:
258 <221> NAME/KEY: VARIANT
259 <222> LOCATION: 6
260 <223> OTHER INFORMATION: Xaa = Y or E
262 <220> FEATURE:
263 <221> NAME/KEY: VARIANT
264 <222> LOCATION: 7
265 <223> OTHER INFORMATION: Xaa = T or S
267 <400> SEQUENCE: 11
W--> 268 Ser Ala Ser Tyr Xaa Xaa Xaa
269      1              5
271 <210> SEQ ID NO: 12
272 <211> LENGTH: 9
273 <212> TYPE: PRT

```

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Input Set : A:\39766-0142 App09602800 saved Dec 21 2005.txt

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```

274 <213> ORGANISM: Mus musculus
276 <400> SEQUENCE: 12
277   Gln Gln Tyr Tyr Ile Tyr Pro Tyr Thr
278       1           5
280 <210> SEQ ID NO: 13
281 <211> LENGTH: 645
282 <212> TYPE: PRT
283 <213> ORGANISM: Homo sapiens
285 <400> SEQUENCE: 13
286   Met Glu Leu Ala Ala Leu Cys Arg Trp Gly Leu Leu Leu Ala Leu
287       1           5           10           15
289   Leu Pro Pro Gly Ala Ala Ser Thr Gln Val Cys Thr Gly Thr Asp
290       20           25           30
292   Met Lys Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met
293       35           40           45
295   Leu Arg His Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu
296       50           55           60
298   Glu Leu Thr Tyr Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln
299       65           70           75
301   Asp Ile Gln Glu Val Gln Gly Tyr Val Leu Ile Ala His Asn Gln
302       80           85           90
304   Val Arg Gln Val Pro Leu Gln Arg Leu Arg Ile Val Arg Gly Thr
305       95          100          105
307   Gln Leu Phe Glu Asp Asn Tyr Ala Leu Ala Val Leu Asp Asn Gly
308      110          115          120
310   Asp Pro Leu Asn Asn Thr Thr Pro Val Thr Gly Ala Ser Pro Gly
311      125          130          135
313   Gly Leu Arg Glu Leu Gln Leu Arg Ser Leu Thr Glu Ile Leu Lys
314      140          145          150
316   Gly Gly Val Leu Ile Gln Arg Asn Pro Gln Leu Cys Tyr Gln Asp
317      155          160          165
319   Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn Asn Gln Leu Ala
320      170          175          180
322   Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys His Pro Cys
323      185          190          195
325   Ser Pro Met Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser Ser Glu
326      200          205          210
328   Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys Ala
329      215          220          225
331   Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys
332      230          235          240
334   Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys
335      245          250          255
337   Leu His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala
338      260          265          270
340   Leu Val Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro
341      275          280          285
343   Glu Gly Arg Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro
344      290          295          300

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 12/28/2005
PATENT APPLICATION: US/09/602,800A TIME: 13:19:50

Input Set : A:\39766-0142 App09602800 saved Dec 21 2005.txt
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:7; Xaa Pos. 10

Seq#:11; Xaa Pos. 5,6,7

VERIFICATION SUMMARY

DATE: 12/28/2005

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Input Set : A:\39766-0142 App09602800 saved Dec 21 2005.txt

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L:214 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7 after pos.:0

L:268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0